

S-2C2

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,254

DATE: 07/16/2002 P-6

TIME: 14:01:35

Input Set : A:\Sequence Listing 1321.2.29.1.txt

Output Set: N:\CRF3\07162002\J009254.raw

3 <110> APPLICANT: University of Utah Research Foundation
 4 Adderson, Elisabeth
 5 Bohnsack, John
 7 <120> TITLE OF INVENTION: Isolated Genes for Virulent Group B Streptococcus agalactiae
 9 <130> FILE REFERENCE: 1321.2.29
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/009,254
 C--> 11 <141> CURRENT FILING DATE: 2001-12-10
 11 <150> PRIOR APPLICATION NUMBER: 60/140,084
 12 <151> PRIOR FILING DATE: 1999-06-21
 14 <160> NUMBER OF SEQ ID NOS: 10
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1509
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Streptococcus agalactiae
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(1509)
 27 <400> SEQUENCE: 1

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30	1 5 10 15	
32	ggt atg gct gta tca cca gtt acg ccg ata gct ttt gcc gct gag aca	96
33	Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr	
34	20 25 30	
36	ggg aca att aca gtt caa gat act caa aaa ggc gca acc tat aaa gca	144
37	Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala	
38	35 40 45	
40	tat aaa gtt ttt gat gca gaa ata gat aat gca aat gta tct gat tcg	192
41	Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser	
42	50 55 60	
44	aat aaa gat gga gct tct tat tta att cct caa ggt aaa gaa gct gag	240
45	Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu	
46	65 70 75 80	
48	tat aaa gct tca act gat ttt aat tct ctt ttt acg aca act act aat	288
49	Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Asn	
50	85 90 95	
52	gga ggg aga aca tat gta act aaa aaa gat act gct tca gca aat gag	336
53	Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu	
54	100 105 110	
56	att gcg aca tgg gct aaa tct ata tca gct aat act aca cca gtt tcc	384
57	Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser	
58	115 120 125	

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61	Thr	Val	Thr	Glu	Ser	Asn	Asn	Asp	Gly	Thr	Glu	Val	Ile	Asn	Val	Ser	
62	130			135								140					
64	caa	tat	gga	tat	tat	ttt	tct	agc	act	gtt	aat	aat	gga	gct	gta		480
65	Gln	Tyr	Gly	Tyr	Tyr	Tyr	Val	Ser	Ser	Thr	Val	Asn	Asn	Gly	Ala	Val	
66	145			150							155				160		
68	att	atg	gtt	aca	tct	gta	act	cca	aat	gct	act	att	cat	gaa	aag	aat	528
69	Ile	Met	Val	Thr	Ser	Val	Thr	Pro	Asn	Ala	Thr	Ile	His	Glu	Lys	Asn	
70				165							170				175		
72	act	gat	gcg	aca	tgg	gga	gat	ggt	gga	aaa	act	gta	gat	caa	aaa		576
73	Thr	Asp	Ala	Thr	Trp	Gly	Asp	Gly	Gly	Lys	Thr	Val	Asp	Gln	Lys		
74				180					185				190				
76	acg	tac	tcg	gtt	ggt	gat	aca	gtc	aaa	tat	act	att	act	tat	aag	aat	624
77	Thr	Tyr	Ser	Val	Gly	Asp	Thr	Val	Lys	Tyr	Thr	Ile	Thr	Tyr	Lys	Asn	
78				195					200				205				
80	gca	gtc	aat	tat	cat	ggt	aca	gaa	aaa	gtg	tat	caa	tat	gtt	ata	aag	672
81	Ala	Val	Asn	Tyr	His	Gly	Thr	Glu	Lys	Val	Tyr	Gln	Tyr	Val	Ile	Lys	
82				210					215				220				
84	gat	act	atg	cca	tct	gct	tct	gta	gtt	gat	ttg	aac	gaa	ggg	tct	tat	720
85	Asp	Thr	Met	Pro	Ser	Ala	Ser	Val	Val	Asp	Leu	Asn	Glu	Gly	Ser	Tyr	
86	225				230						235				240		
88	gaa	gta	act	att	act	gat	gga	tca	ggg	aat	att	aca	act	cta	act	caa	768
89	Glu	Val	Thr	Ile	Thr	Asp	Gly	Ser	Gly	Asn	Ile	Thr	Thr	Leu	Thr	Gln	
90				245						250				255			
92	ggt	tcg	gaa	aaa	gca	act	ggg	aag	tat	aac	ctg	tta	gag	gaa	aat	aat	816
93	Gly	Ser	Glu	Lys	Ala	Thr	Gly	Lys	Tyr	Asn	Leu	Leu	Glu	Glu	Asn	Asn	
94				260						265				270			
96	aat	ttc	acg	att	act	att	ccg	tgg	gca	gct	acc	aat	act	cca	acc	gga	864
97	Asn	Phe	Thr	Ile	Thr	Ile	Pro	Trp	Ala	Ala	Thr	Asn	Thr	Pro	Thr	Gly	
98				275					280				285				
100	aat	act	caa	aat	gga	gct	aat	gat	gac	ttt	ttt	tat	aag	gga	ata	aat	912
101	Asn	Thr	Gln	Asn	Gly	Ala	Asn	Asp	Asp	Phe	Phe	Tyr	Lys	Gly	Ile	Asn	
102				290					295				300				
104	aca	atc	aca	gtc	act	tat	aca	gga	gta	tta	aag	agt	gga	gct	aaa	cca	960
105	Thr	Ile	Thr	Val	Thr	Tyr	Thr	Gly	Val	Leu	Lys	Ser	Gly	Ala	Lys	Pro	
106	305				310						315				320		
108	ggt	tca	gct	gat	tta	cca	gaa	aat	aca	aac	att	gcg	acc	atc	aac	ccc	1008
109	Gly	Ser	Ala	Asp	Leu	Pro	Glu	Asn	Thr	Asn	Ile	Ala	Thr	Ile	Asn	Pro	
110				325						330				335			
112	aat	act	agc	aat	gat	gac	cca	ggg	caa	aaa	gta	aca	gtg	agg	gat	ggt	1056
113	Asn	Thr	Ser	Asn	Asp	Asp	Pro	Gly	Gln	Lys	Val	Thr	Val	Arg	Asp	Gly	
114				340					345				350				
116	caa	att	act	ata	aaa	aaa	att	gat	ggt	tcc	aca	aaa	gct	tca	tta	caa	1104
117	Gln	Ile	Thr	Ile	Lys	Lys	Ile	Asp	Gly	Ser	Thr	Lys	Ala	Ser	Leu	Gln	
118				355					360				365				
120	ggt	gct	ata	ttt	gtt	tta	aag	aat	gct	acg	ggg	caa	ttt	cta	aac	ttt	1152
121	Gly	Ala	Ile	Phe	Val	Leu	Lys	Asn	Ala	Thr	Gly	Gln	Phe	Leu	Asn	Phe	
122				370					375				380				
124	aac	gat	aca	aat	aac	gtt	gaa	tgg	ggc	aca	gaa	gct	aat	gca	aca	gaa	1200

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125	Asn	Asp	Thr	Asn	Asn	Val	Glu	Trp	Gly	Thr	Glu	Ala	Asn	Ala	Thr	Glu
126	385					390				395						400
128	tat	aca	aca	gga	gca	gat	ggt	ata	att	acc	att	aca	ggc	ttg	aaa	gaa
129	Tyr	Thr	Thr	Gly	Ala	Asp	Gly	Ile	Ile	Thr	Ile	Thr	Gly	Leu	Lys	Glu
130						405				410						415
132	ggt	aca	tac	tat	cta	gtt	gag	aaa	aag	gct	ccc	tta	ggt	tac	aat	ttg
133	Gly	Thr	Tyr	Tyr	Leu	Val	Glu	Lys	Lys	Ala	Pro	Leu	Gly	Tyr	Asn	Leu
134						420				425						430
136	tta	gat	aac	tct	cag	aag	gtt	att	tta	gga	gat	gga	gcc	act	gat	acg
137	Leu	Asp	Asn	Ser	Gln	Lys	Val	Ile	Leu	Gly	Asp	Gly	Ala	Thr	Asp	Thr
138						435				440						445
140	act	aat	tca	gat	aac	ctt	tta	gtt	aac	cca	act	gtt	gaa	aat	aac	aaa
141	Thr	Asn	Ser	Asp	Asn	Leu	Leu	Val	Asn	Pro	Thr	Val	Glu	Asn	Asn	Lys
142						450				455						460
144	ggt	act	gag	ttg	cct	tca	aca	ggt	ggt	att	ggt	aca	aca	att	ttc	tac
145	Gly	Thr	Glu	Leu	Pro	Ser	Thr	Gly	Gly	Ile	Gly	Thr	Thr	Ile	Phe	Tyr
146						465				470						480
148	att	ata	ggc	att	tta	gta	ata	ggc	gca	ggt	atc	gtg	ctt	gtt	gct	
149	Ile	Ile	Gly	Ala	Ile	Leu	Val	Ile	Gly	Ala	Gly	Ile	Val	Leu	Val	Ala
150						485				490						495
152	cgt	cgt	cgt	tta	cgt	tct	taa									
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158	<211>	LENGTH:	502													
159	<212>	TYPE:	PRT													
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168	Gly	Met	Ala	Val	Ser	Pro	Val	Thr	Pro	Ile	Ala	Phe	Ala	Ala	Glu	Thr
169						20				25						30
172	Gly	Thr	Ile	Thr	Val	Gln	Asp	Thr	Gln	Lys	Gly	Ala	Thr	Tyr	Lys	Ala
173						35				40						45
176	Tyr	Lys	Val	Phe	Asp	Ala	Glu	Ile	Asp	Asn	Ala	Asn	Val	Ser	Asp	Ser
177						50				55						60
180	Asn	Lys	Asp	Gly	Ala	Ser	Tyr	Leu	Ile	Pro	Gln	Gly	Lys	Glu	Ala	Glu
181		65				70				75						80
184	Tyr	Lys	Ala	Ser	Thr	Asp	Phe	Asn	Ser	Leu	Phe	Thr	Thr	Thr	Asn	
185						85				90						95
188	Gly	Gly	Arg	Thr	Tyr	Val	Thr	Lys	Lys	Asp	Thr	Ala	Ser	Ala	Asn	Glu
189						100				105						110
192	Ile	Ala	Thr	Trp	Ala	Lys	Ser	Ile	Ser	Ala	Asn	Thr	Thr	Pro	Val	Ser
193						115				120						125
196	Thr	Val	Thr	Glu	Ser	Asn	Asn	Asp	Gly	Thr	Glu	Val	Ile	Asn	Val	Ser
197						130				135						140
200	Gln	Tyr	Gly	Tyr	Tyr	Val	Ser	Ser	Thr	Val	Asn	Asn	Gly	Ala	Val	
201		145				150					155					160
204	Ile	Met	Val	Thr	Ser	Val	Thr	Pro	Asn	Ala	Thr	Ile	His	Glu	Lys	Asn

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205	165	170	175
208	Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys		
209	180	185	190
212	Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn		
213	195	200	205
216	Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys		
217	210	215	220
220	Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr		
221	225	230	235
224	Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln		
225	245	250	255
228	Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn		
229	260	265	270
232	Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly		
233	275	280	285
236	Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn		
237	290	295	300
240	Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro		
241	305	310	315
244	Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro		
245	325	330	335
248	Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly		
249	340	345	350
252	Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln		
253	355	360	365
256	Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe		
257	370	375	380
260	Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu		
261	385	390	395
264	Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu		
265	405	410	415
268	Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu		
269	420	425	430
272	Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr		
273	435	440	445
276	Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys		
277	450	455	460
280	Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr		
281	465	470	475
284	Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala		
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289	500		
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293	<211> LENGTH: 1692		
294	<212> TYPE: DNA		
295	<213> ORGANISM: Streptococcus agalactiae		
297	<220> FEATURE:		
298	<221> NAME/KEY: CDS		

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299 <222> LOCATION: (1)..(1692)	
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304 1 5 10 15	
306 att ata tcc aag atc ctt cag gta cat att att ata agt atg att cac	96
307 Ile Ile Ser Lys Ile Leu Gln Val His Ile Ile Ile Ser Met Ile His	
308 20 25 30	
310 gag ata aag atc ccg actcaa cta aag atg cct att ata cga cag ata	144
311 Glu Ile Lys Ile Pro Thr Gln Leu Lys Met Pro Ile Ile Arg Gln Ile	
312 35 40 45	
314 cta gtc tca tca aat gtt gat aca aca act aag tac aag tac gta aaa	192
315 Leu Val Ser Ser Asn Val Asp Thr Thr Lys Tyr Lys Tyr Val Lys	
316 50 55 60	
318 gac gct tac aaa tta gtc ggt tgg tat tat gtt aat cca tat ggt agt	240
319 Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser	
320 65 70 75 80	
322 att aga cct tat aac ttt tca ggt gct gta act caa gat atc aat tta	288
323 Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu	
324 85 90 95	
326 aga gct att tgg cga aag gct gga gat tat cat att ata tac agc aat	336
327 Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn	
328 100 105 110	
330 gat gct gtt ggt aca gat gga aag cca gca ttg gat gct tct ggt cag	384
331 Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln	
332 115 120 125	
334 caa tta caa aca agt aat gag cct act gac cct gat tcc tat gac gat	432
335 Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp	
336 130 135 140	
338 ggc tcc cat tca gcc tta ctg aga cgt ccg aca atg cca gat ggc tat	480
339 Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr	
340 145 150 155 160	
342 cgt ttc cgt ggc tgg tgg tac aat ggt aaa att tat aac cca tat gat	528
343 Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp	
344 165 170 175	
346 tcc att gat att gac gcc cat tta gca gat gct aat aaa aat atc acc	576
347 Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr	
348 180 185 190	
350 ata aaa cct gtc att att cca gta gga gat atc aaa tta gaa gat acc	624
351 Ile Lys Pro Val Ile Ile Pro Val Gly Asp Ile Lys Leu Glu Asp Thr	
352 195 200 205	
354 tcc atc aaa tac aat ggt aac ggt ggt act aga gta gaa aat ggt aat	672
355 Ser Ile Lys Tyr Asn Gly Asn Gly Thr Arg Val Glu Asn Gly Asn	
356 210 215 220	
358 gtg gta aca caa gtg gag aca ccg cgt atg gag ttg aat agc aca act	720
359 Val Val Thr Gln Val Glu Thr Pro Arg Met Glu Leu Asn Ser Thr Thr	
360 225 230 235 240	
362 aca att cct gaa aac caa tac ttt aca agg aca ggt tac aac ctt att	768
363 Thr Ile Pro Glu Asn Gln Tyr Phe Thr Arg Thr Gly Tyr Asn Leu Ile	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 3

VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing 1321.2.29.1.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:655 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0